



SEARCHED LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: ANDERTON, STEPHEN MARK  
VAN DER ZEE, RUURD  
VAN EDEN, WILLEM

(ii) TITLE OF INVENTION: PEPTIDE FRAGMENTS OF MICROBIAL STRESS PROTEINS AND PHARMACEUTICAL COMPOSITION MADE THEREOF FOR THE TREATMENT AND PREVENTION OF INFLAMMATORY DISEASES

(iii) NUMBER OF SEQUENCES: 6

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: THE WEBB LAW FIRM  
(B) STREET: 700 KOPPERS BUILDING, 436 SEVENTH AVENUE  
(C) CITY: PITTSBURGH  
(D) STATE: PENNSYLVANIA  
(E) COUNTRY: UNITED STATES OF AMERICA  
(F) ZIP: 15219-1818

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 3.5" FLOPPY DISK  
(B) COMPUTER: DIGITAL VENTURIS GL 6200  
(C) OPERATING SYSTEM: DOS  
(D) SOFTWARE: MICROSOFT WORD 2.0C

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/716,169  
(B) FILING DATE: 18-SEP-1996

(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: PCT/NL95/00108  
(B) FILING DATE: 21-MAR-1995

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 540  
(B) TYPE: AMINO ACID  
(C) STRANDEDNESS: SINGLE  
(D) TOPOLOGY: UNKNOWN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Met Ala Lys Thr Ile Ala Tyr Asp Glu Glu Ala Arg Arg Gly Leu  
1 5 10 15

Glu Arg Gly Leu Asn Ala Leu Ala Asp Ala Val Lys Val Thr Leu  
20 25 30

Gly Pro Lys Gly Arg Asn Val Val Leu Glu Lys Lys Trp Gly Ala  
35 40 45

Pro Thr Ile Thr Asn Asp Gly Val Ser Ile Ala Lys Glu Ile Glu  
50 55 60

Leu Glu Asp Pro Tyr Glu Lys Ile Gly Ala Glu Leu Val Lys Glu  
65 70 75

Val Ala Lys Lys Thr Asp Asp Val Ala Gly Asp Gly Thr Thr Thr  
80 85 90

Ala Thr Val Leu Ala Gln Ala Leu Val Arg Glu Gly Leu Arg Asn  
95 100 105

Val Ala Ala Gly Ala Asn Pro Leu Gly Val Lys Arg Gly Ile Glu  
110 115 120

Lys Ala Val Glu Lys Val Thr Glu Thr Leu Leu Lys Gly Ala Lys  
125 130 135

Glu Val Glu Thr Lys Glu Gln Ile Ala Ala Thr Ala Ala Ile Ser  
140 145 150

Ala Gly Asp Gln Ser Ile Gly Asp Leu Ile Ala Glu Ala Met Asp  
155 160 165

Lys Val Gly Asn Glu Gly Val Ile Thr Val Glu Glu Ser Asn Thr  
170 175 180

Phe Gly Leu Gln Leu Glu Leu Thr Glu Gly Met Arg Phe Asp Lys  
185 190 195

Gly Tyr Ile Ser Gly Tyr Phe Val Thr Asp Pro Glu Arg Gln Glu  
200 205 210

Ala Val Leu Glu Asp Pro Tyr Ile Leu Leu Val Ser Ser Lys Val  
215 220 225

Ser Thr Val Lys Asp Leu Leu Pro Leu Leu Glu Lys Val Ile Gly  
230 235 240

Ala Gly Lys Pro Leu Leu Ile Ile Ala Glu Asp Val Glu Gly Glu  
245 250 255

Ala Leu Ser Thr Leu Val Val Asn Lys Ile Arg Gly Thr Phe Lys  
260 265 270

Ser Val Ala Val Lys Ala Pro Gly Phe Gly Asp Arg Arg Lys Ala  
275 280 285

Met Leu Gln Asp Met Ala Ile Leu Thr Gly Gly Gln Val Ile Ser  
290 295 300

Glu Glu Val Gly Leu Thr Leu Glu Asn Ala Asp Leu Ser Leu Leu  
305 310 315

Gly Lys Ala Arg Lys Val Val Val Thr Lys Asp Glu Thr Thr Ile  
320 325 330

Val Glu Gly Ala Gly Asp Thr Asp Ala Ile Ala Gly Arg Val Ala  
335 340 345

Gln Ile Arg Gln Glu Ile Glu Asn Ser Asp Ser Asp Tyr Asp Arg  
 350 355 360  
 Glu Lys Leu Gln Glu Arg Leu Ala Lys Leu Ala Gly Gly Val Ala  
 365 370 375  
 Val Ile Lys Ala Gly Ala Ala Thr Glu Val Glu Leu Lys Glu Arg  
 380 385 390  
 Lys His Arg Ile Glu Asp Ala Val Arg Asn Ala Lys Ala Ala Val  
 395 400 405  
 Glu Glu Gly Ile Val Ala Gly Gly Val Thr Leu Leu Gln Ala  
 410 415 420  
 Ala Pro Thr Leu Asp Glu Leu Lys Leu Glu Gly Asp Glu Ala Thr  
 425 430 435  
 Gly Ala Asn Ile Val Lys Val Ala Leu Glu Ala Pro Leu Lys Gln  
 440 445 450  
 Ile Ala Phe Asn Ser Gly Leu Glu Pro Gly Val Val Ala Glu Lys  
 455 460 465  
 Val Arg Asn Leu Pro Ala Gly His Gly Leu Asn Ala Gln Thr Gly  
 470 475 480  
 Val Lys Glu Asp Leu Leu Ala Ala Gly Val Ala Asp Pro Val Lys  
 485 490 495  
 Val Thr Arg Ser Ala Leu Gln Asn Ala Ala Ser Ile Ala Gly Leu  
 500 505 510  
 Phe Leu Thr Thr Glu Ala Val Val Ala Asp Lys Pro Glu Lys Glu  
 515 520 525  
 Lys Ala Ser Val Pro Gly Gly Asp Met Gly Gly Met Asp Phe  
 530 535 540

(3) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 333

(B) TYPE: AMINO ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: UNKNOWN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Ala Val Lys Val Gly Ile Asn Gly Phe Gly Arg Ile Gly Arg Asn  
 1 5 10 15

Val Phe Arg Ala Ala Leu Lys Asn Pro Asp Ile Glu Val Val Ala  
 20 25 30

Val Asn Asp Leu Thr Asp Ala Asn Thr Leu Ala His Leu Leu Lys  
35 40 45

Tyr Asp Ser Val His Gly Arg Leu Asp Ala Glu Val Ser Val Asn  
50 55 60

Gly Asn Asn Leu Val Val Asn Gly Lys Glu Ile Ile Val Lys Ala  
65 70 75

Glu Arg Asp Pro Glu Asn Leu Ala Trp Gly Glu Ile Gly Val Asp  
80 85 90

Ile Val Val Glu Ser Thr Gly Arg Phe Thr Lys Arg Glu Asp Ala  
95 100 105

Ala Lys His Leu Glu Ala Gly Ala Lys Lys Val Ile Ile Ser Ala  
110 115 120

Pro Ala Lys Asn Glu Asp Ile Thr Ile Val Met Gly Val Asn Gln  
125 130 135

Asp Lys Tyr Asp Pro Lys Ala His His Val Ile Ser Asn Ala Ser  
140 145 150

Cys Thr Thr Asn Cys Leu Ala Pro Phe Ala Lys Val Leu His Glu  
155 160 165

Gln Phe Gly Ile Val Arg Gly Met Met Thr Thr Val His Ser Tyr  
170 175 180

Thr Asn Asp Gln Arg Ile Leu Asp Leu Pro His Lys Asp Leu Arg  
185 190 195

Arg Ala Arg Ala Ala Ala Glu Ser Ile Ile Pro Thr Thr Thr Gly  
200 205 210

Ala Ala Lys Ala Val Ala Leu Val Leu Pro Glu Leu Lys Gly Lys  
215 220 225

Leu Asn Gly Met Ala Met Arg Val Pro Thr Pro Asn Val Ser Val  
230 235 240

Val Asp Leu Val Ala Glu Leu Glu Lys Glu Val Thr Val Glu Glu  
245 250 255

Val Asn Ala Ala Leu Lys Ala Ala Ala Glu Gly Glu Leu Lys Gly  
260 265 270

Ile Leu Ala Tyr Ser Glu Glu Pro Leu Val Ser Arg Asp Tyr Asn  
275 280 285

Gly Ser Thr Val Ser Ser Thr Ile Asp Ala Leu Ser Thr Met Val  
290 295 300

Ile Asp Gly Lys Met Val Lys Val Val Ser Trp Tyr Asp Asn Glu  
305 310 315

Thr Gly Tyr Ser His Arg Val Val Asp Leu Ala Ala Tyr Ile Ala  
320 325 330

Ser Lys Gly

(4) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 332

(B) TYPE: AMINO ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: UNKNOWN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Val Lys Val Gly Val Asn Gly Phe Gly Arg Ile Gly Arg Leu Val  
1 5 10 15

Thr Arg Ala Ala Phe Ser Cys Asp Lys Val Asp Ile Val Ala Ile  
20 25 30

Asn Asp Pro Phe Ile Asp Leu Asn Tyr Met Val Tyr Met Phe Gln  
35 40 45

Tyr Asp Ser Thr His Gly Lys Phe Asn Gly Thr Val Lys Ala Glu  
50 55 60

Asn Gly Lys Leu Val Ile Asn Gly Lys Pro Ile Thr Ile Phe Gln  
65 70 75

Glu Arg Asp Pro Val Lys Ile Lys Trp Gly Asp Ala Gly Ala Glu  
80 85 90

Tyr Val Val Glu Ser Thr Gly Val Phe Thr Thr Met Glu Lys Ala  
95 100 105

Gly Ala His Leu Lys Gly Gly Ala Lys Arg Val Ile Ile Ser Ala  
110 115 120

Pro Ser Ala Asp Ala Pro Met Phe Val Met Gly Val Asn His Glu  
125 130 135

Lys Tyr Asp Asn Ser Leu Lys Ile Val Ser Asn Ala Ser Cys Thr  
140 145 150

Thr Asn Cys Leu Ala Pro Leu Ala Lys Val Ile His Asp Asn Phe  
155 160 165

Gly Ile Val Glu Gly Leu Met Thr Thr Val His Ala Ile Thr Ala  
 170 175 180  
 Thr Gln Lys Thr Val Asp Gly Pro Ser Gly Lys Leu Trp Arg Asp  
 185 190 195  
 Gly Arg Gly Ala Ala Gln Asn Ile Ile Pro Ala Ser Thr Gly Ala  
 200 205 210  
 Ala Lys Ala Val Gly Lys Val Ile Pro Glu Leu Asn Gly Lys Leu  
 215 220 225  
 Thr Gly Met Ala Phe Arg Val Pro Thr Pro Asn Val Ser Val Val  
 230 235 240  
 Asp Leu Thr Cys Arg Leu Glu Lys Pro Ala Lys Tyr Asp Asp Ile  
 245 250 255  
 Lys Lys Val Val Lys Gln Ala Ala Glu Gly Pro Leu Lys Gly Ile  
 260 265 270  
 Leu Gly Tyr Thr Glu Asp Gln Val Val Ser Cys Asp Phe Asn Ser  
 275 280 285  
 Asn Ser His Ser Ser Thr Phe Asp Ala Gly Ala Gly Ile Ala Leu  
 290 295 300  
 Asn Asp Asn Ile Val Lys Leu Ile Ser Trp Tyr Asp Asn Glu Tyr  
 305 310 315  
 Gly Tyr Ser Asn Arg Val Val Asp Leu Met Ala Tyr Met Ala Ser  
 320 325 330

Lys Glu

(5) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 573

(B) TYPE: AMINO ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: UNKNOWN

(xi) SEQUENCE DESCRIPTON: SEQ ID NO: 4:

Met Leu Arg Leu Pro Thr Val Phe Arg Gln Met Arg Pro Val Ser  
 1 5 10 15

Arg Val Leu Ala Pro His Leu Thr Arg Ala Tyr Ala Lys Asp Val  
 20 25 30

Lys Phe Gly Ala Asp Ala Arg Ala Leu Met Leu Gln Gly Val Asp  
 35 40 45

Leu Leu Ala Asp Ala Val Ala Val Thr Met Gly Pro Lys Gly Arg  
50 55 60

Thr Val Ile Ile Glu Gln Ser Trp Gly Ser Pro Lys Val Thr Lys  
65 70 75

Asp Gly Val Thr Val Ala Lys Ser Ile Asp Leu Lys Asp Lys Tyr  
80 85 90

Lys Asn Ile Gly Ala Lys Leu Val Gln Asp Val Ala Asn Asn Thr  
95 100 105

Asn Glu Glu Ala Gly Asp Gly Thr Thr Thr Ala Thr Val Leu Ala  
110 115 120

Arg Ser Ile Ala Lys Glu Gly Phe Glu Lys Ile Ser Lys Gly Ala  
125 130 135

Asn Pro Val Glu Ile Arg Arg Gly Val Met Leu Ala Val Asp Ala  
140 145 150

Val Ile Ala Glu Leu Lys Lys Gln Ser Lys Pro Val Thr Thr Pro  
155 160 165

Glu Glu Ile Ala Gln Val Ala Thr Ile Ser Ala Asn Gly Asp Lys  
170 175 180

Glu Ile Gly Asn Ile Ile Ser Asp Ala Met Lys Lys Val Gly Arg  
185 190 195

Lys Gly Val Ile Thr Val Lys Asp Gly Lys Thr Leu Asn Asp Glu  
200 205 210

Leu Glu Ile Ile Glu Gly Met Lys Phe Asp Arg Gly Tyr Ile Ser  
215 220 225

Pro Tyr Phe Ile Asn Thr Ser Lys Gly Gln Lys Cys Glu Phe Gln  
230 235 240

Asp Ala Tyr Val Leu Leu Ser Glu Lys Lys Ile Ser Ser Ile Gln  
245 250 255

Ser Ile Val Pro Ala Leu Glu Ile Ala Asn Ala His Arg Lys Pro  
260 265 270

Leu Val Ile Ile Ala Glu Asp Val Asp Gly Glu Ala Leu Ser Thr  
275 280 285

Leu Val Leu Asn Arg Leu Lys Val Gly Leu Gln Val Val Ala Val  
290 295 300

Lys Ala Pro Gly Phe Gly Asp Asn Arg Lys Asn Gln Leu Lys Asp  
305 310 315

Met Ala Ile Ala Thr Gly Gly Ala Val Phe Gly Glu Glu Gly Leu  
320 325 330

Thr Leu Asn Leu Glu Asp Val Gln Pro His Asp Leu Gly Lys Val  
335 340 345

Gly Glu Val Ile Val Thr Lys Asp Asp Ala Met Leu Leu Lys Gly  
350 355 360

Lys Gly Asp Lys Ala Gln Ile Glu Lys Arg Ile Gln Glu Ile Ile  
365 370 375

Glu Gln Leu Asp Val Thr Thr Ser Glu Tyr Glu Lys Glu Lys Leu  
380 385 390

Asn Glu Arg Leu Ala Lys Leu Ser Asp Gly Val Ala Val Leu Lys  
395 400 405

Val Gly Gly Thr Ser Asp Val Glu Val Asn Glu Lys Lys Asp Arg  
410 415 420

Val Thr Asp Ala Leu Asn Ala Thr Arg Ala Ala Val Glu Glu Gly  
425 430 435

Ile Val Leu Gly Gly Cys Ala Leu Leu Arg Cys Ile Pro Ala  
440 445 450

Leu Asp Ser Leu Thr Pro Ala Asn Glu Asp Gln Lys Ile Gly Ile  
455 460 465

Glu Ile Ile Lys Arg Thr Leu Lys Ile Pro Ala Met Thr Ile Ala  
470 475 480

Lys Asn Ala Gly Val Glu Gly Ser Leu Ile Val Glu Lys Ile Met  
485 490 495

Gln Ser Ser Ser Glu Val Gly Tyr Asp Ala Met Ala Gly Asp Phe  
500 505 510

Val Asn Met Val Glu Lys Gly Ile Ile Asp Pro Thr Lys Val Val  
515 520 525

Arg Thr Ala Leu Leu Asp Ala Ala Gly Val Ala Ser Leu Leu Thr  
530 535 540

Thr Ala Glu Val Val Val Thr Glu Ile Pro Lys Glu Glu Lys Asp  
545 550 555

Pro Gly Met Gly Ala Met Gly Gly Met Gly Gly Gly Met Gly Gly  
560 565 570

Gly Met Phe

(6) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 547

(B) TYPE: AMINO ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: UNKNOWN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Ala Lys Asp Val Lys Phe Gly Ala Asp Ala Arg Ala Leu Met Leu  
1 5 10 15

Gln Gly Val Asp Leu Leu Ala Asp Ala Val Ala Val Thr Met Gly  
20 25 30

Pro Lys Gly Arg Thr Val Ile Ile Glu Gln Ser Trp Gly Ser Pro  
35 40 45

Lys Val Thr Lys Asp Gly Val Thr Val Ala Lys Ser Ile Asp Leu  
50 55 60

Lys Asp Lys Tyr Lys Asn Ile Gly Ala Lys Leu Val Gln Asp Val  
65 70 75

Ala Asn Asn Thr Asn Glu Glu Ala Gly Asp Gly Thr Thr Ala  
80 85 90

Thr Val Leu Ala Arg Ser Ile Ala Lys Glu Gly Phe Glu Lys Ile  
95 100 105

Ser Lys Gly Ala Asn Pro Val Glu Ile Arg Arg Gly Val Met Leu  
110 115 120

Ala Val Asp Ala Val Ile Ala Glu Leu Lys Lys Gln Ser Lys Pro  
125 130 135

Val Thr Thr Pro Glu Glu Ile Ala Gln Val Ala Thr Ile Ser Ala  
140 145 150

Asn Gly Asp Lys Asp Ile Gly Asn Ile Ile Ser Asp Ala Met Lys  
155 160 165

Lys Val Gly Arg Lys Gly Val Ile Thr Val Lys Asp Gly Lys Thr  
170 175 180

Leu Asn Asp Glu Leu Glu Ile Ile Glu Gly Met Lys Phe Asp Arg  
185 190 195

Gly Tyr Ile Ser Pro Tyr Phe Ile Asn Thr Ser Lys Gly Gln Lys  
 200 205 210  
 Cys Glu Phe Gln Asp Ala Tyr Val Leu Leu Ser Glu Lys Lys Ile  
 215 220 225  
 Ser Ser Val Gln Ser Ile Val Pro Ala Leu Glu Ile Ala Asn Ala  
 230 235 240  
 His Arg Lys Pro Leu Val Ile Ala Glu Asp Val Asp Gly Glu  
 245 250 255  
 Ala Leu Ser Thr Leu Val Leu Asn Arg Leu Lys Val Gly Leu Gln  
 260 265 270  
 Val Val Ala Val Lys Ala Pro Gly Phe Gly Asp Asn Arg Lys Asn  
 275 280 285  
 Gln Leu Lys Asp Met Ala Ile Ala Thr Gly Gly Ala Val Phe Gly  
 290 295 300  
 Glu Glu Gly Leu Asn Leu Asn Leu Glu Asp Val Gln Ala His Asp  
 305 310 315  
 Leu Gly Lys Val Gly Glu Val Ile Val Thr Lys Asp Asp Ala Met  
 320 325 330  
 Leu Leu Lys Gly Lys Gly Asp Lys Ala His Ile Glu Lys Arg Ile  
 335 340 345  
 Gln Glu Ile Thr Glu Gln Leu Asp Ile Thr Thr Ser Glu Tyr Glu  
 350 355 360  
 Lys Glu Lys Leu Asn Glu Arg Leu Ala Lys Leu Ser Asp Gly Val  
 365 370 375  
 Ala Val Leu Lys Val Gly Gly Thr Ser Asp Val Glu Val Asn Glu  
 380 385 390  
 Lys Lys Asp Arg Val Thr Asp Ala Leu Asn Ala Thr Arg Ala Ala  
 395 400 405  
 Val Glu Glu Gly Ile Val Leu Gly Gly Cys Ala Leu Leu Arg  
 410 415 420  
 Cys Ile Pro Ala Leu Asp Ser Leu Lys Pro Ala Asn Glu Asp Gln  
 425 430 435  
 Lys Ile Gly Ile Glu Ile Ile Lys Arg Ala Leu Lys Ile Pro Ala  
 440 445 450

(7) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 555

(B) TYPE: AMINO ACID

(B) TYPE: AMINO ACID  
(C) STRANDEDNESS: /SINGLE

(C) STRANDEDNESS: UNKNOWN  
(D) TOPOLOGY: UNKNOWN

(B) TOPOLOGY: UNKNOWN  
(c) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1  
 Ala Pro His Leu Thr Arg Ala Tyr Ala Lys Asp Val Lys Phe Gly  
 1 5 10 15

Ala Asp Ala Arg | Ala Leu Met Leu Gln Gly Val Asp Leu Leu Ala  
20 25 30

Asp Ala Val Ala Val Thr Met Gly Pro Lys Gly Arg Thr Val Ile  
35 40 45

35  
Ile Glu Gln Ser Trp Gly Ser Pro Lys Val Thr Lys Asp Gly Val  
55  
60

50 55  
... Lys Asp Lys Tyr Lys Asp Ile

Thr Val Ala Lys Ser Ile Asp Leu Lys Asp Lys Tyr Lys Asn  
65 70 75

Gly Ala Lys	Leu Val Gln Asp Val Ala Asn Asn Thr Asn Glu Glu		
	80	85	90

Ala Gly Asp | Gly Thr Thr Ala Thr Val Leu Ala Arg Ser Ile  
95 100 105

Ala Lys Glu Gly Phe Glu Lys Ile Ser Lys Gly Ala Asn Pro Val  
110 115 120

Glu Ile Arg Arg Gly Val Met Leu Ala Val Asp Ala Val Ile Ala  
125 130 135

Glu Leu Lys Lys Gln Ser Lys Pro Val Thr Thr Pro Glu Glu Ile  
140 145 150

Ala Gln Val Ala Thr Ile Ser Ala Asn Gly Asp Lys Asp Ile Gly  
155 160 165

Asn Ile Ile Ser Asp Ala Met Lys Lys Val Gly Arg Lys Gly Val  
170 175 180

Ile Thr Val Lys Asp Gly Lys Thr Leu Asn Asp Glu Leu Glu Ile  
185 190 195

Ile Glu Gly Met Lys Phe Asp Arg Gly Tyr Ile Ser Pro Tyr Phe  
200 205 210

Ile Asn Thr Ser Lys Gly Gln Lys Cys Glu Phe Gln Asp Ala Tyr  
215 220 225

Val Leu Leu Ser Glu Lys Lys Phe Ser Ser Val Gln Ser Ile Val  
230 235 240

Pro Ala Leu Glu Ile Ala Asn Ala His Arg Lys Pro Leu Val Ile  
245 250 255

Ile Ala Glu Asp Val Asp Gly Glu Ala Leu Ser Thr Leu Val Leu  
260 265 270

Asn Arg Leu Lys Val Gly Leu Gln Val Val Ala Val Lys Ala Pro  
275 280 285

Gly Phe Gly Asp Asn Arg Lys Asn Gln Leu Lys Asp Met Ala Ile  
290 295 300

Ala Thr Gly Gly Ala Val Phe Gly Glu Glu Gly Leu Asn Leu Asn  
305 310 315

Leu Glu Asp Val Gln Ala His Asp Leu Gly Lys Val Gly Glu Val  
320 325 330

Ile Val Thr Lys Asp Asp Ala Met Leu Leu Lys Gly Lys Gly Asp  
335 340 345

Lys Ala His Ile Glu Lys Arg Ile Gln Glu Ile Thr Glu Gln Leu  
350 355 360

Asp Ile Thr Thr Ser Glu Tyr Glu Lys Glu Lys Leu Asn Glu Arg  
365 370 375

Leu Ala Lys Leu Ser Asp Gly Val Ala Val Leu Lys Val Gly Gly  
380 385 390

Thr Ser Asp Val Glu Val Asn Glu Lys Lys Asp Arg Val Thr Asp  
395 400 405

Ala Leu Asn Ala Thr Arg Ala Ala Val Glu Glu Gly Ile Val Leu  
410 415 420

Gly Gly Gly Cys Ala Leu Leu Arg Cys Ile Pro Ala Leu Asp Ser  
425 430 435

Leu Lys Pro Ala Asn Glu Asp Gln Lys Ile Gly Ile Glu Ile Ile  
440 445 450

Lys Arg Ala Leu Lys Ile Pro Ala Met Thr Ile Ala Lys Asn Ala  
455 460 465

Gly Val Glu Gly Ser Leu Ile Val Glu Lys Ile Leu Gln Ser Ser  
470 475 480

Ser Glu Val Gly Tyr Asp Ala Met Leu Gly Asp Phe Val Asn Met  
485 490 495

Val Glu Lys Gly Ile Ile Asp Pro Thr Lys Val Val Arg Thr Ala  
500 505 510

Leu Leu Asp Ala Ala Gly Val Ala Ser Leu Leu Thr Thr Ala Glu  
515 520 525

Ala Val Val Thr Glu Ile Pro Lys Glu Glu Lys Asp Pro Gly Met  
530 535 540

Gly Ala Met Gly Gly Met Gly Gly Gly Met Gly Gly Gly Met Phe  
545 550 555